

RAW SEQUENCE LISTING

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Application Serial Number: 10/534,894
Source: PCT
Date Processed by STIC: 5-25-05

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/534,894

DATE: 05/25/2005
TIME: 11:40:08

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05252005\J534894.raw

3 <110> APPLICANT: SHANGHAI INSTITUTES FOR BIOLOGICAL SCIENCES, CAS
 5 <120> TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING BALDNESS USING HUMAN AND
 MOUSE RHOR

6 GENE AND CODED PRODUCT THEREOF
 8 <130> FILE REFERENCE: 026816 pc
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/534,894
 C--> 10 <141> CURRENT FILING DATE: 2005-05-13
 10 <150> PRIOR APPLICATION NUMBER: CN 02145353.9
 11 <151> PRIOR FILING DATE: 2002-11-13
 13 <160> NUMBER OF SEQ ID NOS: 14
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2484
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Mus musculus
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(2481)
 25 <223> OTHER INFORMATION:

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 29 atg gcc tca gct gac aag aat ggc agc aac ctc cca tct gtg tct ggt 48
 30 Met Ala Ser Ala Asp Lys Asn Gly Ser Asn Leu Pro Ser Val Ser Gly
 31 1 5 10 15
 33 agc cgc ctg cag agc cgg aag cca ccc aac ctc tcc atc acc atc ccg 96
 34 Ser Arg Leu Gln Ser Arg Lys Pro Pro Asn Leu Ser Ile Thr Ile Pro
 35 20 25 30
 37 cca cca gag agc cag gcc ccc ggc gag cag gat agc atg ctt cct gag 144
 38 Pro Pro Glu Ser Gln Ala Pro Gly Glu Gln Asp Ser Met Leu Pro Glu
 39 35 40 45
 41 agg cgc aag aac cca gcc tac ctg aag agt gtc agc cta cag gag ccc 192
 42 Arg Arg Lys Asn Pro Ala Tyr Leu Lys Ser Val Ser Leu Gln Glu Pro
 43 50 55 60
 45 cgg gga cga tgg cag gag ggc gca gag aag cgc ccc ggc ttc cgc cgc 240
 46 Arg Gly Arg Trp Gln Glu Gly Ala Glu Lys Arg Pro Gly Phe Arg Arg
 47 65 70 75 80
 49 cag gcc tcc ctg tcc cag agc atc cgc aag agc aca gcc cag tgg ttt 288
 50 Gln Ala Ser Leu Ser Gln Ser Ile Arg Lys Ser Thr Ala Gln Trp Phe
 51 85 90 95
 53 ggg gtc agc ggc gac tgg gag ggc aag cga caa aac tgg cat cgt cgc 336
 54 Gly Val Ser Gly Asp Trp Glu Gly Lys Arg Gln Asn Trp His Arg Arg
 55 100 105 110
 57 agc ctg cac cac tgc agc gtg cac tat ggc cgc ctc aag gcc tcg tgc 384
 58 Ser. Leu His His Cys Ser Val His Tyr Gly Arg Leu Lys Ala Ser Cys
 59 115 120 125

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61	cag	aga	gaa	ctg	gag	ctg	ccc	agc	cag	gag	gtg	cca	tcc	ttc	cag	ggc	432
62	Gln	Arg	Glu	Leu	Glu	Leu	Pro	Ser	Gln	Glu	Val	Pro	Ser	Phe	Gln	Gly	
63	130				135						140						
65	act	gag	tct	cca	aaa	ccg	tgc	aag	atg	ccc	aag	att	gtg	gat	cca	ctg	480
66	Thr	Glu	Ser	Pro	Lys	Pro	Cys	Lys	Met	Pro	Lys	Ile	Val	Asp	Pro	Leu	
67	145					150				155			160				
69	gct	cg	gg	t	agg	gcc	ttc	cgc	cat	cca	gat	gag	gtg	gac	cg	cct	528
70	Ala	Arg	Gly	Arg	Ala	Phe	Arg	His	Pro	Asp	Glu	Val	Asp	Arg	Pro	His	
71						165				170			175				
73	gct	gcc	cac	cca	cct	ctg	act	cca	ggg	gtc	ctg	tct	ctc	aca	tcc	ttc	576
74	Ala	Ala	His	Pro	Pro	Leu	Thr	Pro	Gly	Val	Leu	Ser	Leu	Thr	Ser	Phe	
75						180				185			190				
77	acc	agt	gtc	cgc	tct	ggc	tac	tcc	cat	ctg	ccc	cgc	cgc	aag	agg	ata	624
78	Thr	Ser	Val	Arg	Ser	Gly	Tyr	Ser	His	Leu	Pro	Arg	Arg	Lys	Arg	Ile	
79						195				200			205				
81	tct	gtt	gcc	cat	atg	agc	ttt	cag	gca	gcc	gcc	ctc	ctc	aag	ggg		672
82	Ser	Val	Ala	His	Met	Ser	Phe	Gln	Ala	Ala	Ala	Leu	Leu	Lys	Gly		
83						210				215			220				
85	cgt	tcc	gt	ct	a	gt	gc	act	ggg	cag	cgg	tgc	cg	cat	gtc	aaa	520
86	Arg	Ser	Val	Leu	Asp	Ala	Thr	Gly	Gln	Arg	Cys	Arg	His	Val	Lys	Arg	
87						225				230			235			240	
89	agc	t	tc	g	c	cc	agc	ttc	ctg	gag	gag	gat	gct	gtc	gat	gga	768
90	Ser	Phe	Ala	Tyr	Pro	Ser	Phe	Leu	Glu	Glu	Asp	Ala	Val	Asp	Gly	Ala	
91						245				250			255				
93	gac	acc	t	tc	g	ac	tcc	ttt	ttt	agt	aag	gaa	gaa	atg	agc	tcc	816
94	Asp	Thr	Phe	Asp	Ser	Ser	Phe	Phe	Ser	Lys	Glu	Glu	Met	Ser	Ser	Met	
95						260				265			270				
97	cct	gac	gat	gtc	ttt	gag	tcc	ccc	cca	ctc	tct	gcc	agc	tac	ttc	cg	864
98	Pro	Asp	Asp	Val	Phe	Glu	Ser	Pro	Pro	Leu	Ser	Ala	Ser	Tyr	Phe	Arg	
99						275				280			285				
101	gg	t	gt	cc	ca	c	c	t	cc	cc	gt	cc	cac	atc		912	
102	Gly	Val	Pro	His	Ser	Ala	Ser	Pro	Val	Ser	Pro	Asp	Gly	Val	His	Ile	
103						290				295			300				
105	ccg	cta	aaa	gaa	tac	agc	gg	gg	gc	cc	ctg	gg	ccc	ggg	acc	cag	960
106	Pro	Leu	Lys	Glu	Tyr	Ser	Gly	Gly	Arg	Ala	Leu	Gly	Pro	Gly	Thr	Gln	
107						305				310			315			320	
109	cgt	gg	aaa	cgc	att	gcc	tcc	aaa	gta	aag	cac	ttt	gca	ttt	gac	cg	1008
110	Arg	Gly	Lys	Arg	Ile	Ala	Ser	Lys	Val	Lys	His	Phe	Ala	Phe	Asp	Arg	
111						325				330			335				
113	aag	aag	agg	cac	tac	gg	cc	tt	gt	gt	gg	tt	g	cc	tt	cc	1056
114	Lys	Lys	Arg	His	Tyr	Gly	Leu	Gly	Val	Val	Gly	Asn	Trp	Leu	Asn	Arg	
115						340				345			350				
117	agc	tat	cga	cgc	agc	atc	agc	agc	acc	gt	cag	cg	cg	cag	ttc	gg	1104
118	Ser	Tyr	Arg	Arg	Ser	Ile	Ser	Ser	Thr	Val	Gln	Arg	Gln	Leu	Glu	Ser	
119						355				360			365				
121	t	tc	g	at	agc	cac	cg	cc	tac	tac	t	gg	ct	ac	tt	cac	1152
122	Phe	Asp	Ser	His	Arg	Pro	Tyr	Phe	Thr	Tyr	Trp	Leu	Thr	Phe	Val	His	
123						370				375			380				
125	atc	atc	atc	acc	tt	tg	gt	atc	tgc	acc	tat	gg	cc	atc	gt		1200

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126 Ile Ile Ile Thr Leu Leu Val Ile Cys Thr Tyr Gly Ile Ala Pro Val	
127 385 390 395 400	
129 ggc ttt gcc cag cac gtt acc acc cag ctg gtg ctg aag aac aga ggc	1248
130 Gly Phe Ala Gln His Val Thr Thr Gln Leu Val Leu Lys Asn Arg Gly	
131 405 410 415	
133 gtg tat gag agc gtg aag tac atc cag cag gag aac ttc tgg att ggc	1296
134 Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu Asn Phe Trp Ile Gly	
135 420 425 430	
137 ccc agc tcg att gac ctc att cac ctg gga gca aag ttc tcg ccc tgc	1344
138 Pro Ser Ser Ile Asp Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys	
139 435 440 445	
141 atc cg ^g aag gac cag caa att gag cag ctg gta cg ^g agg gag cg ^c gac	1392
142 Ile Arg Lys Asp Gln Gln Ile Glu Gln Leu Val Arg Arg Glu Arg Asp	
143 450 455 460	
145 att gag cg ^c acc tct ggc tgc tgt gtc cag aat gac cg ^c tcg ggc tgc	1440
146 Ile Glu Arg Thr Ser Gly Cys Cys Val Gln Asn Asp Arg Ser Gly Cys	
147 465 470 475 480	
149 atc cag acc ctg aag aag gac tgc tcg gag act tta gcc acg ttc gta	1488
150 Ile Gln Thr Leu Lys Lys Asp Cys Ser Glu Thr Leu Ala Thr Phe Val	
151 485 490 495	
153 aag tgg cag aat gat act ggg ccc tca gac aag tct gac ctg acg cag	1536
154 Lys Trp Gln Asn Asp Thr Gly Pro Ser Asp Lys Ser Asp Leu Ser Gln	
155 500 505 510	
157 aag cag cca tcg gcg gtt gtg tgc cac caa gac ccc agg acc tgt gaa	1584
158 Lys Gln Pro Ser Ala Val Val Cys His Gln Asp Pro Arg Thr Cys Glu	
159 515 520 525	
161 gag cct gcc tcc agt ggg gcc cac atc tgg cct gat gac att acc aag	1632
162 Glu Pro Ala Ser Ser Gly Ala His Ile Trp Pro Asp Asp Ile Thr Lys	
163 530 535 540	
165 tgg ccg atc tgc aca gag cag gct cag acg aac cac acg ggc ttg ttg	1680
166 Trp Pro Ile Cys Thr Glu Gln Ala Gln Ser Asn His Thr Gly Leu Leu	
167 545 550 555 560	
169 cac ata gac tgt aag atc aaa ggc cg ^c ccc tgc tgc atc ggc acc aag	1728
170 His Ile Asp Cys Lys Ile Lys Gly Arg Pro Cys Cys Ile Gly Thr Lys	
171 565 570 575	
173 ggc agc tgc gag atc acc act cgg gag tac tgt gag ttc atg cat ggc	1776
174 Gly Ser Cys Glu Ile Thr Thr Arg Glu Tyr Cys Glu Phe Met His Gly	
175 580 585 590	
177 tat ttc cat gaa gac gcg acg ctg tgt tcc cag gtg cac tgt tta gac	1824
178 Tyr Phe His Glu Asp Ala Thr Leu Cys Ser Gln Val His Cys Leu Asp	
179 595 600 605	
181 aag gtg tgt ggg ctc ctg cct ttc ctc aac cct gag gtc cct gac cag	1872
182 Lys Val Cys Gly Leu Leu Pro Phe Leu Asn Pro Glu Val Pro Asp Gln	
183 610 615 620	
185 ttc tac ccg atc tgg ctg tct tta ttc ctg cat gct ggc ata gtg cac	1920
186 Phe Tyr Arg Ile Trp Leu Ser Leu Phe Leu His Ala Gly Ile Val His	
187 625 630 635 640	
189 tgc ctt gtg tct gtg gtc ttc caa atg acc atc ctg agg gac cta gag	1968
190 Cys Leu Val Ser Val Val Phe Gln Met Thr Ile Leu Arg Asp Leu Glu	

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191	645	650	655	
193	aag ctg gcc ggc tgg cac cgc atc tcc atc atc atc ctt agt ggc			2016
194	Lys Leu Ala Gly Trp His Arg Ile Ser Ile Ile Phe Ile Leu Ser Gly			
195	660	665	670	
197	att aca ggc aac ctg gcc agc gcc atc ttc ctc ccc tac cgg gca gag			2064
198	Ile Thr Gly Asn Leu Ala Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu			
199	675	680	685	
201	gtg ggc cca gcc ggg tcg cag ttc ggc ctc ctc gcc tgc ctc ttc gtg			2112
202	Val Gly Pro Ala Gly Ser Gln Phe Gly Leu Leu Ala Cys Leu Phe Val			
203	690	695	700	
205	gag ctg ttc cag agc tgg cag ctg ttg gag cgg ccg tgg aag gcc ttc			2160
206	Glu Leu Phe Gln Ser Trp Gln Leu Leu Glu Arg Pro Trp Lys Ala Phe			
207	705	710	715	720
209	ttc aac ctg tcg gcc att gtg ctt ttc ctc atc tgt ggc ctc ctg			2208
210	Phe Asn Leu Ser Ala Ile Val Leu Phe Leu Phe Ile Cys Gly Leu Leu			
211	725	730	735	
213	ccc tgg ata gac aac atc gcc cac atc ttc ggg ttc ctc agc ggc atg			2256
214	Pro Trp Ile Asp Asn Ile Ala His Ile Phe Gly Phe Leu Ser Gly Met			
215	740	745	750	
217	ctt ctg gcc ttc gcc ttc ctg cct tac att acc ttc ggc acc agc gac			2304
218	Leu Leu Ala Phe Ala Phe Leu Pro Tyr Ile Thr Phe Gly Thr Ser Asp			
219	755	760	765	
221	aag tac cgc aag cga gcc ctc atc ctc gtg tcg ctg ctg gtc ttt gct			2352
222	Lys Tyr Arg Lys Arg Ala Leu Ile Leu Val Ser Leu Leu Val Phe Ala			
223	770	775	780	
225	ggg ctc ttt gct tcc ctg gtg ctg tgg ctg tac atc tac ccc atc aac			2400
226	Gly Leu Phe Ala Ser Leu Val Leu Trp Leu Tyr Ile Tyr Pro Ile Asn			
227	785	790	795	800
229	tgg ccc tgg atc gag tac ctc acc tgc ttt ccc ttc acc agc cgc ttc			2448
230	Trp Pro Trp Ile Glu Tyr Leu Thr Cys Phe Pro Phe Thr Ser Arg Phe			
231	805	810	815	
233	tgt gag aag tac gag cta gac cag gtg cta cac taa			2484
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239	<211> LENGTH: 827			
240	<212> TYPE: PRT			
241	<213> ORGANISM: Mus musculus			
243	<400> SEQUENCE: 2			
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250	20	25	30	
253	Pro Pro Glu Ser Gln Ala Pro Gly Glu Gln Asp Ser Met Leu Pro Glu			
254	35	40	45	
257	Arg Arg Lys Asn Pro Ala Tyr Leu Lys Ser Val Ser Leu Gln Glu Pro			
258	50	55	60	
261	Arg Gly Arg Trp Gln Glu Gly Ala Glu Lys Arg Pro Gly Phe Arg Arg			
262	65	70	75	80

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265 Gln Ala Ser Leu Ser Gln Ser Ile Arg Lys Ser Thr Ala Gln Trp Phe
266 85 90 95
269 Gly Val Ser Gly Asp Trp Glu Gly Lys Arg Gln Asn Trp His Arg Arg
270 100 105 110
273 Ser Leu His His Cys Ser Val His Tyr Gly Arg Leu Lys Ala Ser Cys
274 115 120 125
277 Gln Arg Glu Leu Glu Leu Pro Ser Gln Glu Val Pro Ser Phe Gln Gly
278 130 135 140
281 Thr Glu Ser Pro Lys Pro Cys Lys Met Pro Lys Ile Val Asp Pro Leu
282 145 150 155 160
285 Ala Arg Gly Arg Ala Phe Arg His Pro Asp Glu Val Asp Arg Pro His
286 165 170 175
289 Ala Ala His Pro Pro Leu Thr Pro Gly Val Leu Ser Leu Thr Ser Phe
290 180 185 190
293 Thr Ser Val Arg Ser Gly Tyr Ser His Leu Pro Arg Arg Lys Arg Ile
294 195 200 205
297 Ser Val Ala His Met Ser Phe Gln Ala Ala Ala Leu Leu Lys Gly
298 210 215 220
301 Arg Ser Val Leu Asp Ala Thr Gly Gln Arg Cys Arg His Val Lys Arg
302 225 230 235 240
305 Ser Phe Ala Tyr Pro Ser Phe Leu Glu Glu Asp Ala Val Asp Gly Ala
306 245 250 255
309 Asp Thr Phe Asp Ser Ser Phe Phe Ser Lys Glu Glu Met Ser Ser Met
310 260 265 270
313 Pro Asp Asp Val Phe Glu Ser Pro Pro Leu Ser Ala Ser Tyr Phe Arg
314 275 280 285
317 Gly Val Pro His Ser Ala Ser Pro Val Ser Pro Asp Gly Val His Ile
318 290 295 300
321 Pro Leu Lys Glu Tyr Ser Gly Gly Arg Ala Leu Gly Pro Gly Thr Gln
322 305 310 315 320
325 Arg Gly Lys Arg Ile Ala Ser Lys Val Lys His Phe Ala Phe Asp Arg
326 325 330 335
329 Lys Lys Arg His Tyr Gly Leu Gly Val Val Gly Asn Trp Leu Asn Arg
330 340 345 350
333 Ser Tyr Arg Arg Ser Ile Ser Ser Thr Val Gln Arg Gln Leu Glu Ser
334 355 360 365
337 Phe Asp Ser His Arg Pro Tyr Phe Thr Tyr Trp Leu Thr Phe Val His
338 370 375 380
341 Ile Ile Ile Thr Leu Leu Val Ile Cys Thr Tyr Gly Ile Ala Pro Val
342 385 390 395 400
345 Gly Phe Ala Gln His Val Thr Thr Gln Leu Val Leu Lys Asn Arg Gly
346 405 410 415
349 Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu Asn Phe Trp Ile Gly
350 420 425 430
353 Pro Ser Ser Ile Asp Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys
354 435 440 445
357 Ile Arg Lys Asp Gln Gln Ile Glu Gln Leu Val Arg Arg Glu Arg Asp
358 450 455 460
361 Ile Glu Arg Thr Ser Gly Cys Cys Val Gln Asn Asp Arg Ser Gly Cys

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:28 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25